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09/762224

#4



PUR-115:JJS:133252

SEQUENCE LISTING

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Sharkey, Curtis Matthew  
North, Cynthia Lin  
Fishbach, Michael A.

<120> PSEUDOTYPED RETROVIRUSES AND STABLE CELL LINES FOR THEIR PRODUCTION  
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<140> US 09/762,224  
<141> 2001-02-02  
<150> PCT/US99/17702  
<151> 1999-08-04  
<150> U.S. 60/095,242  
<151> 1998-08-04  
<150> U.S. 60/112,405  
<151> 1998-12-15  
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<213> Alphavirus Ross River virus  
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Cys Ser Ser Pro Pro Cys Tyr Pro Cys Cys Tyr Glu Lys Gln Pro Glu	
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Gln Thr Leu Arg Met Leu Glu Asp Asn Val Asn Arg Pro Gly Tyr Tyr	
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Glu Leu Leu Glu Ala Ser Met Thr Cys Arg Asn Arg Ser Arg His Arg	
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Arg Ser Val Thr Glu His Phe Asn Val Tyr Lys Ala Thr Arg Pro Tyr	
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Leu Ala Tyr Cys Ala Asp Cys Gly Asp Gly Tyr Phe Cys Tyr Ser Pro	
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gtt gct atc gag aag atc cga gat gag gcg tct gac ggc atg ctc aag	336
Val Ala Ile Glu Lys Ile Arg Asp Glu Ala Ser Asp Gly Met Leu Lys	
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atc caa gtc tcc gcc caa ata ggt ctg gac aag gca ggt acc cac gcc	384
Ile Gln Val Ser Ala Gln Ile Gly Leu Asp Lys Ala Gly Thr His Ala	
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His Thr Lys Ile Arg Tyr Met Ala Gly His Asp Val Gln Glu Ser Lys	
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Arg Asp Ser Leu Arg Val Tyr Thr Ser Ala Ala Cys Ser Ile His Gly	
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Thr Met Gly His Phe Ile Val Ala His Cys Pro Pro Gly Asp Tyr Leu	
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Lys Val Ser Phe Glu Asp Ala Asp Ser His Val Lys Ala Cys Lys Val	
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Gln Tyr Lys His Asp Pro Leu Pro Val Gly Arg Glu Lys Phe Val Val	
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Arg Pro His Phe Gly Val Glu Leu Pro Cys Thr Ser Tyr Gln Leu Thr	
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Thr Ala Pro Thr Asp Glu Glu Ile Asp Met His Thr Pro Pro Asp Ile	
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275 280 285																				
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325 330 335																				
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Ala Leu Thr Pro Gly Ala Val Val Pro Leu Thr Leu Gly Leu Leu Cys																				
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500 505 510	
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Pro Tyr Lys Ala His Ile Glu Arg Asn Gly Phe Ser Pro Met Thr Leu	
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595 600 605	
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Cys Cys Gly Thr Ser Glu Cys Ser Ser Lys Glu Gln Pro Asp Tyr Gln	
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Cys Lys Val Tyr Thr Gly Val Tyr Pro Phe Met Trp Gly Gly Ala Tyr	
625 630 635 640	
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645 650 655	
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Arg Ser Asp Val Cys Lys His Asp His Ala Ser Ala Tyr Lys Ala His	
660 665 670	
acg gcc tct cta aaa gca aca atc agg atc agt tat ggc acc atc aac	2064
Thr Ala Ser Leu Lys Ala Thr Ile Arg Ile Ser Tyr Gly Thr Ile Asn	
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Gln Thr Thr Glu Ala Phe Val Asn Gly Glu His Ala Val Asn Val Gly	
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725 730 735	
cca ccc tac gga tca ggc cag ccg ggt aga ttc gga gac att cag agc	2256
Pro Pro Tyr Gly Ser Gly Gln Pro Gly Arg Phe Gly Asp Ile Gln Ser	
740 745 750	
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Arg Thr Val Glu Ser Lys Asp Leu Tyr Ala Asn Thr Ala Leu Lys Leu	
755 760 765	
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Ser Arg Pro Ser Pro Gly Val Val His Val Pro Tyr Thr Gln Thr Pro	
770 775 780	
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Asp Cys Ala Val Gly Ser Ile Pro Val Ser Met Asp Ile Pro Asp Ser	
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Gln Val Val Val Cys Thr His Ser Ser Asp Phe Gly Gly Val Ala Thr	
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Leu Ser Tyr Lys Thr Asp Lys Pro Gly Lys Cys Ala Val His Ser His	
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Ser Asn Val Ala Thr Leu Gln Glu Ala Thr Val Asp Val Lys Glu Asp	
885 890 895	
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Gly Lys Val Thr Val His Phe Ser Thr Ala Ser Ala Ser Pro Ala Phe	
900 905 910	
aaa gtg tcc gtc tgt gac gca aaa aca acg tgc acg gcg gcg tgc gag	2784
Lys Val Ser Val Cys Asp Ala Lys Thr Thr Cys Thr Ala Ala Cys Glu	
915 920 925	
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Pro Pro Lys Asp His Ile Val Pro Tyr Gly Ala Ser His Asn Asn Gln  
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gtc ttt ccg gac atg tca gga act gcg atg acg tgg gtg cag agg ctg 2880  
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gcc agt ggg tta ggt ggg ctg gct ctc atc gcg gtg gtt gtg ctg gtc 2928  
 Ala Ser Gly Leu Gly Gly Leu Ala Leu Ile Ala Val Val Val Leu Val  
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<212> DNA

<213> Filovirus Ebola virus, subtype Zaire

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agg aca tca ttc ttt ctt tgg gta att atc ctt ttc caa aga aca ttt 103  
 Arg Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe  
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tcc atc cca ctt gga gtc atc cac aat agc aca tta cag gtt agt gat 151  
 Ser Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp  
 35 40 45

gtc gac aaa cta gtt tgt cgt gac aaa ctg tca tcc aca aat caa ttg 199  
 Val Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu  
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aga tca gtt gga ctg aat ctc gaa ggg aat gga gtg gca act gac gtg 247  
 Arg Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val  
 65 70 75

cca tct gca act aaa aga tgg ggc ttc agg tcc ggt gtc cca cca aag 295  
 Pro Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys  
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gtg gtc aat tat gaa gct ggt gaa tgg gct gaa aac tgc tac aat ctt 343  
 Val Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu  
 100 105 110

gaa atc aaa aaa cct gac ggg agt gag tgt cta cca gca gcg cca gac 391  
 Glu Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp  
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ggg aga aga act cga aga gaa gca att gtc aat gct caa ccc aaa tgc Gly Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys 505 510 515	1495
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Thr Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp	
585 590 595	
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Phe Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp	
600 605 610	
tgc tgt atc gaa cca cat gat tgg acc aag aac ata aca gac aaa att	1831
Cys Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile	
615 620 625	
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Asp Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly	
630 635 640	
gac aat gac aat tgg tgg aca gga tgg aga caa tgg ata ccg gca ggt	1927
Asp Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly	
645 650 655 660	
att gga gtt aca ggc gtt ata att gca gtt atc gct tta ttc tgt ata	1975
Ile Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile	
665 670 675	
tgc aaa ttt gtc ttt tag tttttcttca gattgcttca tggaaaagct cagcctcaaa	2033
Cys Lys Phe Val Phe	
680	
tcaatgaaac caggatttaa ttatatggat tacttgaatc taagattact tgacaaatga	2093
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<211> 2103

<212> DNA

<213> Filovirus Marburg

<400> 3

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aca aaa aat ctc ccc att tta gag ata gct agt aat aat caa ccc caa	102
thr lys asn leu pro ile leu glu ile ala ser asn asn gln pro gln	
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aat gtg gat tcg gta tgc tcc gga act ctc cag aag aca gaa gac gtc	150
asn val asp ser val cys ser gly thr leu gln lys thr glu asp val	
35 40 45	

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aac atc cgt gac tat cct aaa tgc aaa act atc cat cat att caa ggt asn ile arg asp tyr pro lys cys lys thr ile his his ile gln gly 115 120 125	390
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gac act gga tgt ttc ggc gct ctt caa gaa tac aat tct aca aag aac asp thr gly cys phe gly ala leu gln glu tyr asn ser thr lys asn 210 215 220	678
caa aca tgt gct ccg tcc aaa ata cct cca cca ctg ccc aca gcc cgt gln thr cys ala pro ser lys ile pro pro pro leu pro thr ala arg 225 230 235 240	726
ccg gag atc aaa ctc aca agc acc cca act gat gcc acc aaa ctc aat pro glu ile lys leu thr ser thr pro thr asp ala thr lys leu asn 245 250 255	774
acc acg gac cca agc agt gat gat gag gac ctc gca aca tcc ggc tca thr thr asp pro ser ser asp asp glu asp leu ala thr ser gly ser 260 265 270	822
ggg tcc gga gaa cga gaa ccc cac aca act tct gat gcg gtc acc aag	870

gly	ser	gly	glu	arg	glu	pro	his	thr	thr	ser	asp	ala	val	thr	lys	
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caa	ggg	ctt	tca	tca	aca	atg	cca	ccc	act	ccc	tca	cca	caa	cca	agc	918
gln	gly	leu	ser	ser	thr	met	pro	pro	thr	pro	ser	pro	gln	pro	ser	
	290					295				300						
acg	cca	cag	caa	gga	gga	aac	aac	aca	aac	cat	tcc	caa	gat	gct	gtg	966
thr	pro	gln	gln	gly	gly	asn	asn	thr	asn	his	ser	gln	asp	ala	val	
305				310					315						320	
act	gaa	cta	gac	aaa	aat	aac	aca	act	gca	caa	ccg	tcc	atg	ccc	cct	1014
thr	glu	leu	asp	lys	asn	asn	thr	thr	ala	gln	pro	ser	met	pro	pro	
				325					330					335		
cat	aac	act	acc	aca	atc	tct	act	aac	aac	acc	tcc	aaa	cac	aac	ttc	1062
his	asn	thr	thr	thr	ile	ser	thr	asn	asn	thr	ser	lys	his	asn	phe	
			340				345						350			
agc	act	ctc	tct	gca	cca	tta	caa	aac	acc	acc	aat	gac	aac	aca	cag	1110
ser	thr	leu	ser	ala	pro	leu	gln	asn	thr	thr	asn	asp	asn	thr	gln	
	355					360					365					
agc	aca	atc	act	gaa	aat	gag	caa	acc	agt	gcc	ccc	tcg	ata	aca	acc	1158
ser	thr	ile	thr	glu	asn	glu	gln	thr	ser	ala	pro	ser	ile	thr	thr	
	370					375				380						
ctg	cct	cca	acg	gga	aat	ccc	acc	aca	gca	aag	agc	acc	agc	agc	aaa	1206
leu	pro	pro	thr	gly	asn	pro	thr	thr	ala	lys	ser	thr	ser	ser	lys	
385				390					395						400	
aaa	ggc	ccc	gcc	aca	acg	gca	cca	aac	acg	aca	aat	gag	cat	ttc	acc	1254
lys	gly	pro	ala	thr	thr	ala	pro	asn	thr	thr	asn	glu	his	phe	thr	
			405			410							415			
agt	cct	ccc	ccc	acc	ccc	agc	tcg	act	gca	caa	cat	ctt	gta	tat	ttc	1302
ser	pro	pro	pro	thr	pro	ser	ser	thr	ala	gln	his	leu	val	tyr	phe	
			420			425						430				
aga	aga	aag	cga	agt	atc	ctc	tgg	agg	gaa	ggc	gac	atg	ttc	cct	ttt	1350
arg	arg	lys	arg	ser	ile	leu	trp	arg	glu	gly	asp	met	phe	pro	phe	
		435				440					445					
ctg	gat	ggg	tta	ata	aat	gct	cca	att	gat	ttt	gac	cca	gtt	cca	aat	1398
leu	asp	gly	leu	ile	asn	ala	pro	ile	asp	phe	asp	pro	val	pro	asn	
	450				455				460							
aca	aaa	aca	atc	ttt	gat	gaa	tcc	tct	agt	tct	ggt	gcc	tcg	gct	gag	1446
thr	lys	thr	ile	phe	asp	glu	ser	ser	ser	ser	gly	ala	ser	ala	glu	
465				470					475					480		
gaa	gat	caa	cat	gcc	tcc	ccc	aat	att	agt	tta	act	tta	tct	tat	ttt	1494
glu	asp	gln	his	ala	ser	pro	asn	ile	ser	leu	thr	leu	ser	tyr	phe	
			485			490						495				
cct	aat	ata	aat	gag	aac	act	gcc	tac	tct	gga	gaa	aat	gag	aat	gat	1542
pro	asn	ile	asn	glu	asn	thr	ala	tyr	ser	gly	glu	asn	glu	asn	asp	

500	505	510	
tgt gat gca gag tta aga att tgg agc gtt cag gag gat gac ctg gcc			1590
cys asp ala glu leu arg ile trp ser val gln glu asp asp leu ala			
515	520	525	
gca ggg ctc agt tgg ata ccg ttt ttt ggc cct gga att gaa gga ctt			1638
ala gly leu ser trp ile pro phe phe gly pro gly ile glu gly leu			
530	535	540	
tac act gct gtt tta att aaa aat caa aac aat ttg gtc tgc agg ttg			1686
tyr thr ala val leu ile lys asn gln asn asn leu val cys arg leu			
545	550	555	560
agg cgt cta gcc aat caa act gcc aaa tcc ttg gaa ctc tta ttg aga			1734
arg arg leu ala asn gln thr ala lys ser leu glu leu leu leu arg			
565	570	575	
gtc aca act gag gaa aga aca ttc tcc tta atc aat aga cat gct att			1782
val thr thr glu glu arg thr phe ser leu ile asn arg his ala ile			
580	585	590	
gac ttt cta ctc aca aga tgg gga gga aca tgc aaa gtg ctt gga cct			1830
asp phe leu leu thr arg trp gly gly thr cys lys val leu gly pro			
595	600	605	
gat tgt tgc atc ggg ata gaa gac ttg tcc aaa aat att tca gag caa			1878
asp cys cys ile gly ile glu asp leu ser lys asn ile ser glu gln			
610	615	620	
att gac caa att aaa aag gac gaa caa aaa gag ggg act ggt tgg ggt			1926
ile asp gln ile lys lys asp glu gln lys glu gly thr gly trp gly			
625	630	635	640
ctg ggt ggt aaa tgg tgg aca tcc gac tgg ggt gtt ctt act aac ttg			1974
leu gly gly lys trp trp thr ser asp trp gly val leu thr asn leu			
645	650	655	
ggc att ttg cta cta tta tcc ata gct gtc ttg att gct cta tcc tgt			2022
gly ile leu leu leu leu ser ile ala val leu ile ala leu ser cys			
660	665	670	
att tgt cgt atc ttt act aaa tat atc gga taa cggtta aatgtgtaat gattaggact			2080
ile cys arg ile phe thr lys tyr ile gly			
675	680		
ttaggacaat tgctactgag ccc			2103